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between two markers where the LOD score was the greatest.

[Results]

Tables 1, 2, and 3 show the results for the DHHS population, RI1 population, and RI2 population, respectively. In Tables 1 through 3, "Population" denotes the name of a population subjected to the QTL analysis, "Trait" means characteristic, "Chromosome" means the chromosome on which the genetic markers are located, "Marker interval (M1-A-QTL-B-M2)" means two genetic markers flanking a QTL in the vicinity thereof, "Distance (cM) A+B" means the distance between two genetic markers flanking a QTL, "Position^{a)} (cM)A" means the distance between genetic marker M1 and QTL, "Position (cM)B" means the distance between genetic marker M2 and QTL, "LOD^{b)} Score" means the peak value of LOD score, "Var. (%)^{c)}" is the value that indicates what proportion (%) of the phenotype variance is accounted for by the presence of a QTL, and "Weight^{d)}" is the value indicative of the margin by which the score for barley resistance to yellow mosaic disease is increased due to the presence of a QTL.